STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 128784

TO: Ilia Ouspenski **Location: 3d74 / 3c70** **Tuesday, August 10, 2004** **Art Unit: 1644** **Phone: 272-2920** **Serial Number: 10 / 790396**	**From: Jan Delaval** **Location: Biotech-Chem Library** **Rem 1A51** **Phone: 272-2504** **jan.delaval@uspto.gov**

Search Notes

Access DB# 128750

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner # :_____ Date: _____
Art Unit: _____ Phone Number 30_____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

****

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher: am	NA Sequence (#) ✓	STN _____
Searcher Phone #: 22504	AA Sequence (#) ✓	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: 8/3	Bibliographic _____	Dr.Link _____
Date Completed: 8/10	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems ✓
Clerical Prep Time: 20	Patent Family _____	WWW/Internet _____
Online Time: +20	Other _____	Other (specify) _____

PTO-1590 (8-01)

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Qy         16 ACTATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTCTATGGTGCTGCTTCC 75
Db          7 ThrMetGlyLeuSerHisThrLeuLeuValMetAlaLeuLeuLeuSerGlyValSerSer 26

Qy         76 ATGAAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGCCATTTTACAAATTCT 135
Db         27 MetLysSerGlnAlaTyrPheAsnLysThrGlyGluLeuProCysHisPheThrAsnSer 46

Qy        136 CAAAACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAGGATAAGCTGGTTCTG 195
Db         47 GlnAsnIleSerLeuAspGluLeuValValPheTrpGlnAspGlnAspLysLeuValLeu 66

Qy        196 TACGAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGCAAGTATAAGGGCCGC 255
Db         67 TyrGluIlePheArgGlyLysGluAsnProGlnAsnValHisLeuLysTyrLysGlyArg 86

Qy        256 ACAAGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATTCAGATCAAGGACAAG 315
Db         87 ThrSerPheAspLysAspAsnTrpThrLeuArgLeuHisAsnValGlnIleLysAspLys 106

Qy        316 GGCTTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTCGTTCCCATGCACCAG 375
Db        107 GlyThrTyrHisCysPheIleHisTyrLysGlyProLysGlyLeuValProMetHisGln 126

Qy        376 ATGAATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAAATAATGGTAACTTCT 435
Db        127 MetSerSerAspLeuSerValLeuAlaAsnPheSerGlnProGluIleThrValThrSer 146

Qy        436 AATAGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCCATACAAGGTTACCCA 495
Db        147 AsnArgThrGluAsnSerGlyIleIleAsnLeuThrCysSerSerIleGlnGlyTyrPro 166

Qy        496 GAACCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTAAGTATGATACT 555
Db        167 GluProLysGluMetTyrPheGlnLeuAsnThrGluAsnSerThrThrLysTyrAspThr 186

Qy        556 GTCATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTTTCTATCAGCTTGTCC 615
Db        187 ValMetLysLysSerGlnAsnAsnValThrGluLeuTyrAsnValSerIleSerLeuPro 206

Qy        616 TTCTCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGTCCTGCAACTTGAGTCAATG 675
Db        207 PheSerValProGluAlaHisAsnValSerValPheCysAlaLeuLysLeuGluThrLeu 226

Qy        676 AAG---CTTCCCTCCCTACCTTATAATATAGATGCACATACGAAA---CCCACCCCTGAT 729
Db        227 GluMetLeuLeuSerLeuProPheAsnIleAspAlaGlnProLysAspLysAspProGlu 246

Qy        730 GGAGACCACATCCTCTGGATTGCGGCTCTGCTTGTAATGTTGGTCATTTTGTGTGGGATG 789
Db        247 GlnGlyHisPheLeuTrpIleAlaAlaValLeuValMetPheValValPheCysGlyMet 266

Qy        790 GTGTTCTTTCTAACACTAAGGAAAAGGAAGAAGAAGCAGCCTGGCCCCTCTCATGAATGT 849
Db        267 ValSerPheLysThrLeuArgLysArgLysLysLysGlnProGlyProSerHisGluCys 286

Qy        850 GAAACCAACAAAGTGGAGAGAAAAGAAAGTGAGCAGACCAAGGAAAGAGTACGGTACCAT 909
Db        287 GluThrIleLysArgGluArgLysGluSerLysGlnThrAsnGluArgValProTyrHis 306

Qy        910 GAAACGGAAAGATCTGATGAAGCCCAGTGTGTTAACATTTCGAAGACAGCTTCAGGCGAC 969
Db        307 ValProGluArgSerAspGluAlaGlnCysValAsnIleLeuLysThrAlaSerGlyAsp 326

Qy        970 AACAGT 975
Db        327 LysAsn 328

RESULT 6
O02838
ID   O02838      PRELIMINARY;      PRT;   325 AA.
AC   O02838;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   B7-2.
GN   CD86.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97047772; PubMed=8892613;
RA   Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,
RA   Bothwell A.L.;
RT   "Porcine endothelial CD86 is a major costimulator of xenogeneic human
RT   T cells: cloning, sequencing, and functional expression in human
RT   endothelial cells.";
RL   J. Immunol. 157:3838-3844(1996).
DR   EMBL; L76099; AAB61307.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   325 AA;  36527 MW;  988BE08137B0597D CRC64;

Alignment Scores:
Pred. No.:              5.16e-107      Length:          325
Score:                  1199.00        Matches:         239
Percent Similarity:     82.42%         Conservative:    33
Best Local Similarity:  72.42%         Mismatches:      46
Query Match:            68.63%         Indels:          12
DB:                     6              Gaps:            7

US-10-790-396-9 (1-987) x O02838 (1-325)

Qy         19 ATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTCTATGGTGCTGCTTCCATG 78
Db          1 MetGlyLeuSerAsnIleLeuPheValMetValLeuLeuLeuSerGlyAlaAlaSerLeu 20

Qy         79 AAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGCCATTTTACAAATTCTCAA 138
Db         21 LysSerGlnAlaTyrPheAsnGluThrGlyGluLeuProCysHisPheThrAsnSerGln 40

Qy        139 AACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAGGATAAGCTGGTTCTGTAC 198
Db         41 AsnLeuSerLeuAspGluLeuValIlePheTrpGlnAspGlnAspAsnLeuValLeuTyr 60

Qy        199 GAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGCAAGTATAAGGGCCGCACA 258
Db         61 GluLeuTyrArgGlyGlnGluLysProHisAsnValAsnSerLysTyrMetGlyArgThr 80

Qy        259 AGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATTCAGATCAAGGACAAGGGC 318
Db         81 SerPheAspGlnAlaThrTrpThrLeuArgLeuHisAsnValGlnIleLysAspLysGly 100

Qy        319 TTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTCGTTCCCATGCACCAGATG 378
Db        101 SerTyrGlnCysPheIleHisHisLysGlyProHisGlyLeuValProIleHisGlnMet 120

Qy        379 AATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAAATAATGGTAACTTCTAAT 438
Db        121 SerSerAspLeuSerLeuLeuAlaAsnPheSerGlnProGluIleAsnLeuLeuThrAsn 140

Qy        439 AGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCCATACAAGGTTACCCAGAA 498
Db        141 HisThrGluAsnSer---ValIleAsnLeuThrCysSerSerThrGlnGlyTyrProGlu 159

Qy        499 CCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTAAGTATGATACTGTC 558
Db        160 ProGlnArgMetTyrMetLeuLeuAsnThrLysAsnSerThrThrGluHisAspAlaAsp 179

Qy        559 ATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTTTCTATCAGCTTGTCCTTC 618
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Db        180 MetLysLysSerGlnAsnAsnIleThrGluLeuTyrAsnValSerIleArgValSerLeu 199

Qy        619 TCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGTCCTGCAACTTGAGTCAATGAAG 678
                 :::|||      :::||||||||||||   ||||||||||||||||||      |||
Db        200 ProIleProProGluThrAsnValSerIleValCysValLeuGlnLeuGluProSerLys 219

Qy        679 ------CTTCCCTCCCTACCTTATAATATAGATGCACATACGAAACCC---------ACC 723
                   |||   |||||||||   ||||||||||||      ||||||
Db        220 ThrLeuLeuPheSerLeuProCysAsnIleAspAla------LysProProValGlnPro 237

Qy        724 CCTGATGGAGACCACATCCTCTGGATTGCGGCTCTGCTTGTAATGTTGGTCATTTTGTGT 783
              |||      ||||||||||||||||||||||||||||||||   :::|||:::::|||
Db        238 ProValProAspHisIleLeuTrpIleAlaAlaLeuLeuValThrValValValValCys 257

Qy        784 GGGATGGTGTTCTTTCTAACACTAAGGAAAAGGAAGAAGAAGCAGCCTGGCCCCTCTCAT 843
              |||||||||   |||:::||||||||||||||||||||||||||||||||||||:::
Db        258 GlyMetValSerPheValThrLeuArgLysArgLysLysLysGlnProGlyProSerAsn 277

Qy        844 GAATGT---GAAACCAACAAAGTGGAGAGAAAAGAAAGTGAGCAGACCAAGGAAAGAGTA 900
              ||||||   ||||||   |||:::   ||||||   ||||||||||||||   |||
Db        278 GluCysGlyGluThrIleLysMetAsnArgLysAlaSerGluGlnThrLysAsnArgAla 297

Qy        901 CGGTACCATGAAACGGAAAGATCTGATGAAGCCCAGTGT---GTTAACATTTCGAAGACA 957
                  |||      ||||||||||||:::|||||||||   |||||||||   ||||||
Db        298 GluValHis------GluArgSerAspAspAlaGlnCysAspValAsnIleLeuLysThr 315

Qy        958 GCTTCAGGCGACAACAGTACTACACAGTTT 987
              ||||||   ||||||||||||||   |||
Db        316 AlaSerAspAspAsnSerThrThrAspPhe 325

RESULT 7
Q9BDM4
ID   Q9BDM4      PRELIMINARY;      PRT;   323 AA.
AC   Q9BDM4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD86 protein precursor.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
DR   EMBL; AF344857; AAK37540.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Signal.
FT   SIGNAL        1     17       POTENTIAL.
SQ   SEQUENCE   323 AA;  37019 MW;  D211E103DB1A7D7A CRC64;

Alignment Scores:
Pred. No.:              7.47e-86        Length:         323
Score:                  980.00          Matches:        202
Percent Similarity:     76.38%          Conservative:   47
Best Local Similarity:  61.96%          Mismatches:     71
Query Match:            56.10%          Indels:         6
DB:                     6               Gaps:           6

US-10-790-396-9 (1-987) x Q9BDM4 (1-323)

Qy         19 ATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTCTATGGTGCTGCTTCCATG 78
              |||   |||:::|||||||||||||||||||      ||||||   |||||||||   :::
Db          1 MetGlyLeuSerAsnIleLeuPheValMetAlaPheLeuLeuSerGlyAlaAlaProLeu 20

Qy         79 AAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGCCATTTTACAAATTCTCAA 138
              |||   |||||||||||||||:::|||   :::|||||||||   |||   |||||||||
Db         21 LysIleGlnAlaTyrPheAsnGluThrAlaAspLeuProCysGlnPheAlaAsnSerGln 40

Qy        139 AACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAGGATAAGCTGGTTCTGTAC 198
              |||   ||||||   |||||||||||||||||||||:::|||:::   |||||||||
Db         41 AsnArgSerLeuSerGluLeuValValPheTrpGlnAsnGlnGluAsnLeuValLeuAsn 60

Qy        199 GAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGCAAGTATAAGGGCCGCACA 258
              |||:::|||   |||||||||          :::|||||||   ||||||   |||||||||
Db         61 GluValTyrLeuGlyLysGluLysPheAspSerValHisSerLysTyrMetGlyArgThr 80

Qy        259 AGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATTCAGATCAAGGACAAGGGC 318
              |||||||||   ::::::|||||||||||||||||||||:::|||||||||||||||||
Db         81 SerPheAspProGluSerTrpThrLeuArgLeuHisAsnLeuGlnIleLysAspLysGly 100

Qy        319 TTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTCGTTCCCATGCACCAGATG 378
              ||||||||||||   :::|||||||||   |||   |||::::::   :::|||||||||
Db        101 LeuTyrGlnCysIleIleHisHisLysArgProThrGlyMetIleArgIleHisGlnMet 120

Qy        379 AATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAAATAATGGTAACTTCTAAT 438
              ||||||:::|||||||||||||||||||||||||||||||||||:::      ||||||
Db        121 AsnSerGluLeuSerValLeuAlaAsnPheSerGlnProGluIleValProIleSerAsn 140

Qy        439 AGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCCATACAAGGTTACCCAGAA 498
              |||||||||          ||||||||||||||||||||||||   ||||||||||||
Db        141 IleThrGluAsnMet---TyrIleAsnLeuThrCysSerSerIleHisGlyTyrProGlu 159

Qy        499 CCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTAAGTATGATACTGTC 558
              |||::::::|||      |||:::::::|||:||||||:::   :::|||||   |||
Db        160 ProGluLysMetSerValLeuLeuArgThrLysAsnSerThrIleGluTyrAspGlyVal 179

Qy        559 ATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTTTCTATCAGCTTGTCCTTC 618
              |||:::|||||||||:::|||||||||||||||||||:::|||||||||||||||||
Db        180 MetGlnLysSerGlnAspAsnValThrGluLeuTyrAspValSerIleSerLeuSerVal 199

Qy        619 TCAGTCCCTGAA---GCAAGCAATGTGAGCATCTTCTGTGTCCTGCAACTTGAGTCAATG 675
              |||   |||:::      ||||||:::::|||||||||||||:::   :::
Db        200 SerPheProAspValThrSerAsnMetThrIlePheCysValLeuGluThrAspLysThr 219

Qy        676 AAGCTTCCCTCCCTACCTTATAATATAGATGCACATACGAAACCCACCCCTGATGGAGAC 735
              :::|||   |||   |||::::::|||:::            |||   |||      |||
Db        220 GlnLeuLeuSerSerProPheSerIleGluLeuGlu---AspProGlnProProProAsp 238

Qy        736 CACATCCTCTGGATTGCGGCTCTGCTTGTAATGTTGGTCATTTTGTGTGGGATGGTGTTC 795
              ||||||   ||||||   |||:::|||          ||||||:::|||   |||   |||
Db        239 HisIleProTrpIleThrAlaValLeu---ProThrValIleIleCysValMetAlaPhe 257

Qy        796 TTTCTAACACTAAGGAAA---AGGAAGAAGAAGCAGCCTGGCCCCTCTCATGAATGTGAA 852
              |||   |||   |||   :::|||||||||||||||      |||:::::|||
Db        258 CysLeuIleLeuTrpLysTrpLysLysLysLysGlnProArgAsnSerTyrLysCysGly 277

Qy        853 ACCAACAAAGTGGAGAGAAAAGAAAGTGAGCAGACCAAGGAAAGAGTACGGTACCATGAA 912
              ||||||   :::|||||||:::|||||||||||||||||:::|||   :::   :::
Db        278 ThrAsnThrMetGluArgGluGluSerGluGlnThrLysLysArgGluLysIleAsnVal 297

Qy        913 ACGGAAAGATCTGATGAAGCCCAGTGTGTTAACATTTCG---AAGACAGCTTCAGGCGAC 969
              |||||||||||||||||||||||||||      |||   ||||||   |||   |||
Db        298 ProGluArgSerAspGluAlaGlnCysValPheLysSerLeuLysThrProSerCysAsp 317

Qy        970 AACAGTACTACACAGTTT 987
                 |||   |||:::|||
Db        318 LysSerAspThrArgPhe 323

RESULT 8
Q9BDB8
ID   Q9BDB8      PRELIMINARY;      PRT;   323 AA.
AC   Q9BDB8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD86 protein precursor.
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Qy        196 TACGAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGCAAGTATAAGGGCCGC 255
              ||||||::::::|||||||||||||||||||||||||||||||   ||||||||||||||||
Db         67 TyrGluIlePheArgGlyLysGluAsnProGlnAsnValHisLeuLysTyrLysGlyArg 86

Qy        256 ACAAGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATTCAGATCAAGGACAAG 315
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db         87 ThrSerPheAspLysAspAsnTrpThrLeuArgLeuHisAsnValGlnIleLysAspLys 106

Qy        316 GGCTTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTCGTTCCCATGCACCAG 375
              |||   |||   ||||||:::|||:::|||||||||||||||||||||||||||||||||
Db        107 GlyThrTyrHisCysPheIleHisTyrLysGlyProLysGlyLeuValProMetHisGln 126

Qy        376 ATGAATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAAATAATGGTAACTTCT 435
              |||:::|||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        127 MetSerSerAspLeuSerValLeuAlaAsnPheSerGlnProGluIleThrValThrSer 146

Qy        436 AATAGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCCATACAAGGTTACCCA 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AsnArgThrGluAsnSerGlyIleIleAsnLeuThrCysSerSerIleGlnGlyTyrPro 166

Qy        496 GAACCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTAAGTATGATACT 555
              ||||||||||||||||||||   :::   ||||||||||||:::|||||||||||||||
Db        167 GluProLysGluMetTyrPheGlnLeuAsnThrGluAsnSerThrThrLysTyrAspThr 186

Qy        556 GTCATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTTTCTATCAGCTTGTCC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ValMetLysLysSerGlnAsnAsnValThrGluLeuTyrAsnValSerIleSerLeuPro 206

Qy        616 TTCTCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGTCCTGCAACTTGAGTCAATG 675
              ||||||||||||||||   |||||||||:::||||||   |||:::||||||:::::::
Db        207 PheSerValProGluAlaHisAsnValSerValPheCysAlaLeuLysLeuGluThrLeu 226

Qy        676 AAG---CTTCCCTCCCTACCTTATAATATA---------------------------- 702
              :::   |||   |||||||||:::||||||
Db        227 GluMetLeuLeuSerLeuProPheAsnIleAspAlaGlnProLysAspLysAspProGlu 246

Qy        702 ------------------------------------------------------------ 702

Db        247 GlnGlyHisPheLeuTrpIleAlaAlaValLeuValMetPheValValPheCysGlyMet 266

Qy        702 ------------------------------------------------------------ 702

Db        267 ValSerPheLysThrLeuArgLysArgLysLysLysGlnProGlyProSerHisGluCys 286

Qy        703 GAAACCAACAAAGTGGAGAGAAAAGAAAGTGAGCAGACCAAGGAAAGAGTACGGTACCAT 762
              ||||||   |||   |||||||||||||||:::||||||   |||||||||   ||||||
Db        287 GluThrIleLysArgGluArgLysGluSerLysGlnThrAsnGluArgValProTyrHis 306

Qy        763 GAAACGGAAAGATCTGATGAAGCCCAGTGTGTTAACATTTCGAAGACAGCTTCAGGCGAC 822
                  ||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        307 ValProGluArgSerAspGluAlaGlnCysValAsnIleLeuLysThrAlaSerGlyAsp 326

Qy        823 AACAGT 828
                 :::
Db        327 LysAsn 328
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RESULT 6
O02838
ID O02838 PRELIMINARY; PRT; 325 AA.
AC O02838;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE B7-2.
GN CD86.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97047772; PubMed=8892613;
RA Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,
RA Bothwell A.L.;
RT "Porcine endothelial CD86 is a major costimulator of xenogeneic human
RT T cells: cloning, sequencing, and functional expression in human
RT endothelial cells.";
RL J. Immunol. 157:3838-3844(1996).
DR EMBL; L76099; AAB61307.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 325 AA; 36527 MW; 988BE08137B0597D CRC64;

Alignment Scores:

Pred. No.:	1.01e-82	Length:	325
Score:	996.50	Matches:	202
Percent Similarity:	70.12%	Conservative:	28
Best Local Similarity:	61.59%	Mismatches:	41
Query Match:	67.47%	Indels:	57
DB:	6	Gaps:	5

US-10-790-396-19 (1-840) x O02838 (1-325)

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Qy         19 ATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTCTATGGTGCTGCTTCCATG 78
              |||   |||:::|||||||||||||||||||   |||||||||   ||||||||||:::
Db          1 MetGlyLeuSerAsnIleLeuPheValMetValLeuLeuLeuSerGlyAlaAlaSerLeu 20

Qy         79 AAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGCCATTTTACAAATTCTCAA 138
              ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db         21 LysSerGlnAlaTyrPheAsnGluThrGlyGluLeuProCysHisPheThrAsnSerGln 40

Qy        139 AACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAGGATAAGCTGGTTCTGTAC 198
              |||:::|||||||||||||||||:::|||||||||||||||||||   ||||||||||||
Db         41 AsnLeuSerLeuAspGluLeuValIlePheTrpGlnAspGlnAspAsnLeuValLeuTyr 60

Qy        199 GAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGCAAGTATAAGGGCCGCACA 258
              ||||||||||||||:::|||   |||   ||||||:::   ||||||   |||||||||
Db         61 GluLeuTyrArgGlyGlnGluLysProHisAsnValAsnSerLysTyrMetGlyArgThr 80

Qy        259 AGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATTCAGATCAAGGACAAGGGC 318
              |||||||||:::      ||||||||||||||||||||||:::||||||||||||||||||
Db         81 SerPheAspGlnAlaThrTrpThrLeuArgLeuHisAsnValGlnIleLysAspLysGly 100

Qy        319 TTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTCGTTCCCATGCACCAGATG 378
                 ||||||||||:::|||||||||||||||   ||||||||||||:::|||||||||
Db        101 SerTyrGlnCysPheIleHisHisLysGlyProHisGlyLeuValProIleHisGlnMet 120

Qy        379 AATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAAATAATGGTAACTTCTAAT 438
              :::|||||||||||:::|||||||||||||||||||||||||||||||   :::   :::|||
Db        121 SerSerAspLeuSerLeuLeuAlaAsnPheSerGlnProGluIleAsnLeuLeuThrAsn 140

Qy        439 AGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCCATACAAGGTTACCCAGAA 498
                 ||||||||||||   :::|||||||||||||||||||||||   ||||||||||||||||
Db        141 HisThrGluAsnSer---ValIleAsnLeuThrCysSerSerThrGlnGlyTyrProGlu 159

Qy        499 CCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTAAGTATGATACTGTC 558
              |||:::   ||||||   |||:::   |||:::|||||||:::|||:::::::|||
Db        160 ProGlnArgMetTyrMetLeuLeuAsnThrLysAsnSerThrThrGluHisAspAlaAsp 179

Qy        559 ATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTTTCTATCAGCTTGTCCTTC 618
              ||||||||||||||||||||:::|||||||||||||||||||||||||||   :::|||
Db        180 MetLysLysSerGlnAsnAsnIleThrGluLeuTyrAsnValSerIleArgValSerLeu 199

Qy        619 TCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGTCCTGCAACTTGAGTCAATGAAG 678
                 :::|||      :::||||||||||||   ||||||||||||||||||      |||
Db        200 ProIleProProGluThrAsnValSerIleValCysValLeuGlnLeuGluProSerLys 219

Qy        679 ------CTTCCCTCCCTACCTTATAATATA---------------------------- 702
                    |||   |||||||||   ||||||
Db        220 ThrLeuLeuPheSerLeuProCysAsnIleAspAlaLysProProValGlnProProVal 239

Qy        702 ------------------------------------------------------------ 702
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Db        240 ProAspHisIleLeuTrpIleAlaAlaLeuLeuValThrValValValValCysGlyMet 259

Qy        702 ------------------------------------------------------------ 702

Db        260 ValSerPheValThrLeuArgLysArgLysLysLysGlnProGlyProSerAsnGluCys 279

Qy        703 ---GAAACCAACAAAGTGGAGAGAAAAGAAAGTGAGCAGACCAAGGAAAGAGTACGGTAC 759
                  ||||||   |||:::   ||||||   ||||||||||||||||   |||
Db        280 GlyGluThrIleLysMetAsnArgLysAlaSerGluGlnThrLysAsnArgAlaGluVal 299

Qy        760 CATGAAACGGAAAGATCTGATGAAGCCCAGTGT---GTTAACATTTCGAAGACAGCTTCA 816
                  |||      ||||||||||||:::|||||||||   |||||||||   ||||||||||||
Db        300 His------GluArgSerAspAspAlaGlnCysAspValAsnIleLeuLysThrAlaSer 317

Qy        817 GGCGACAACAGTACTACACAGTTT 840
                  ||||||||||||||   |||
Db        318 AspAspAsnSerThrThrAspPhe 325

RESULT 7
Q9BDN9
ID   Q9BDN9      PRELIMINARY;      PRT;   275 AA.
AC   Q9BDN9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD86 protein precursor.
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Papio.
OX   NCBI_TaxID=9555;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
DR   EMBL; AF344836; AAK37532.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Signal.
FT   SIGNAL        1     17       POTENTIAL.
SQ   SEQUENCE   275 AA;  31343 MW;  3AAD3481B4F37C19 CRC64;

Alignment Scores:
Pred. No.:              3.42e-72       Length:        275
Score:                  881.50         Matches:       176
Percent Similarity:     78.99%         Conservative:  42
Best Local Similarity:  63.77%         Mismatches:    55
Query Match:            59.68%         Indels:        3
DB:                     6              Gaps:          3

US-10-790-396-19 (1-840) x Q9BDN9 (1-275)

Qy         19 ATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTCTATGGTGCTGCTTCCATG 78
              |||   |||:::|||||||||||||||||||      ||||||   |||||||||   :::
Db          1 MetGlyLeuSerAsnIleLeuPheValMetAlaPheLeuLeuSerGlyAlaAlaProLeu 20

Qy         79 AAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGCCATTTTACAAATTCTCAA 138
              |||   ||||||||||||||:::|||   :::|||||||||   |||   |||||||||
Db         21 LysIleGlnAlaTyrPheAsnGluThrAlaAspLeuProCysGlnPheAlaAsnSerGln 40

Qy        139 AACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAGGATAAGCTGGTTCTGTAC 198
              |||   ||||||   ||||||||||||||||||||:::|||:::   |||||||||
Db         41 AsnArgSerLeuSerGluLeuValValPheTrpGlnAsnGlnGluAsnLeuValLeuAsn 60

Qy        199 GAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGCAAGTATAAGGGCCGCACA 258
              |||:::|||   |||:::|||          :::||||||   ||||||   |||||||||
Db         61 GluValTyrLeuGlyArgGluLysPheAspSerValHisSerLysTyrMetGlyArgThr 80

Qy        259 AGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATTCAGATCAAGGACAAGGGC 318
              |||||||||   ::::::||||||||||||||||||||:::|||||||||||||||||
Db         81 SerPheAspProGluSerTrpThrLeuArgLeuHisAsnLeuGlnIleLysAspLysGly 100

Qy        319 TTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTCGTTCCCATGCACCAGATG 378
              ||||||||||||   :::|||||||||   |||   |||::::::   :::|||||||||
Db        101 LeuTyrGlnCysIleIleHisHisLysArgProThrGlyMetIleArgIleHisGlnMet 120

Qy        379 AATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAAATAATGGTAACTTCTAAT 438
              ||||||:::|||||||||||||||||:::|||||||||||||||||:::      ||||||
Db        121 AsnSerGluLeuSerValLeuAlaSerPheSerGlnProGluIleValProIleSerAsn 140

Qy        439 AGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCCATACAAGGTTACCCAGAA 498
              |||||||||         |||||||||||||||||||||||||   ||||||||||||
Db        141 IleThrGluAsnMet---TyrIleAsnLeuThrCysSerSerIleHisGlyTyrProGlu 159

Qy        499 CCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTAAGTATGATACTGTC 558
              |||::::::|||      |||::::::|||:::|||||:::   :::||||||   |||
Db        160 ProGluLysMetSerValLeuLeuArgThrLysAsnSerThrIleGluTyrAspGlyVal 179

Qy        559 ATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTTTCTATCAGCTTGTCCTTC 618
              |||:::|||||||||:::|||||||||||||||||||:::|||||||||||||||||||
Db        180 MetGlnLysSerGlnAspAsnValThrGluLeuTyrAspValSerIleSerLeuSerVal 199

Qy        619 TCAGTCCCTGAA---GCAAGCAATGTGAGCATCTTCTGTGTCCTGCAACTTGAGTCAATG 675
              |||   |||:::      ||||||:::::|||||||||||||||:::   :::
Db        200 SerProAspValThrSerAsnMetThrIlePheCysValLeuGluThrAspLysThr 219

Qy        676 AAGCTTCCCTCCCTACCTTATAATATAGAAACCAACAAAGTGGAGAGAAAAGAAAGTGAG 735
              :::|||   |||   |||::::::|||   ||||||   :::|||||:::|||||||||
Db        220 GlnLeuLeuSerSerProPheSerIleGlyThrAsnThrMetGluArgGluGluSerGlu 239

Qy        736 CAGACCAAGGAAAGAGTACGGTACCATGAAACGGAAAGATCTGATGAAGCCCAGTGTGTT 795
              |||||||||:::|||   :::   :::      ||||||||||||||||||||||||||||
Db        240 GlnThrLysLysArgGluLysIleAsnValProGluArgSerAspGluAlaGlnCysVal 259

Qy        796 AACATTTCG---AAGACAGCTTCAGGCGACAACAGTACTACACAGTTT 840
              |||   ||||||   |||   |||   |||   |||   |||
Db        260 PheLysSerLeuLysThrProSerCysAspLysSerAspThrHisPhe 275

RESULT 8
Q9BDM4
ID   Q9BDM4      PRELIMINARY;      PRT;   323 AA.
AC   Q9BDM4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD86 protein precursor.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
DR   EMBL; AF344857; AAK37540.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Signal.
FT   SIGNAL        1     17       POTENTIAL.
SQ   SEQUENCE   323 AA;  37019 MW;  D211E103DB1A7D7A CRC64;

Alignment Scores:
Pred. No.:              1.55e-70       Length:        323
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                     IQGYPEPKEMYFLVKTENSSTKYDTVMKKSQNNVTELYNVSISLSFSVPEASNVSIFC
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                     TTQF"
     3'UTR           850. .1795
                     /gene="CD86"
ORIGIN

  Query Match           71.3%;  Score 704;  DB 4;  Length 1795;
  Best Local Similarity   99.3%;  Pred. No. 2e-178;
  Matches  707;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGTATCTCAGATGCACTATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 ATGTATCTCAGATGCACTATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTC 66

Qy         61 TATGGTGCTGCTTCCATGAAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TATGGTGCTGCTTCCATGAAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGC 126

Qy        121 CATTTTACAAATTCTCAAAACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CATTTTACAAATTCTCAAAACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAG 186

Qy        181 GATAAGCTGGTTCTGTACGAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GATAAGCTGGTTCTGTACGAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGC 246

Qy        241 AAGTATAAGGGCCGCACAAGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AAGTATAAGGGCCGCACAAGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATT 306

Qy        301 CAGATCAAGGACAAGGGCTTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CAGATCAAGGACAAGGGCTTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTC 366

Qy        361 GTTCCCATGCACCAGATGAATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GTTCCCATGCACCAGATGAATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAA 426

Qy        421 ATAATGGTAACTTCTAATAGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 ATAATGGTAACTTCTAATAGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCC 486

Qy        481 ATACAAGGTTACCCAGAACCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 ATACAAGGTTACCCAGAACCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGT 546

Qy        541 ACTAAGTATGATACTGTCATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 ACTAAGTATGATACTGTCATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTT 606

Qy        601 TCTATCAGCTTGTCCTTCTCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGTCCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 TCTATCAGCTTGTCCTTCTCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGTCCTG 666

Qy        661 CAACTTGAGTCAATGAAGCTTCCCTCCCTACCTTATAATATAGATGCACATA 712
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CAACTTGAGTCAATGAAGCTTCCCTCCCTACCTTATAATATAGAAACCAACA 718


RESULT 8
PIGCD86G
LOCUS       PIGCD86G                994 bp    mRNA    linear   MAM 17-JUN-1997
DEFINITION  Sus scrofa CD86 mRNA, complete cds.
ACCESSION   L76099
VERSION     L76099.1  GI:2198558
KEYWORDS    T cell costimulation.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 994)
  AUTHORS   Maher,S.E., Karmann,K., Min,W., Hughes,C.C., Pober,J.S. and
            Bothwell,A.L.
  TITLE     Porcine endothelial CD86 is a major costimulator of xenogeneic
            human T cells: cloning, sequencing, and functional expression in
            human endothelial cells
  JOURNAL   J. Immunol. 157 (9), 3838-3844 (1996)
  MEDLINE   97047772
   PUBMED   8892613
COMMENT     GSDB:S:74002
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9823"
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                     /cell_type="endothelial"
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     3'UTR           979. .994
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                     /gene="CD86"
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ORIGIN

  Query Match           62.8%;  Score 620;  DB 4;  Length 994;
  Best Local Similarity   81.3%;  Pred. No. 8.7e-156;
  Matches  800;  Conservative    0;  Mismatches  160;  Indels   24;  Gaps    6;

Qy         19 ATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTCTATGGTGCTGCTTCCATG 78
              |||| ||||| ||||||||||||||||||. |||||||||| |||||||| ||| ||
Db          1 ATGGGACTGAGTAACATTCTCTTTGTGATGGTCCTCCTGCTCTCTGGTGCTGCCTCCTTG 60

Qy         79 AAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGCCATTTTACAAATTCTCAA 138
              || ||||| |||||||||||  |||||||||||||||| |||||||||||||| || ||
Db         61 AAAAGTCAGGCATATTTCAATGAGACTGGAGAACTGCCGTGCCATTTTACAAACTCGCAG 120

Qy        139 AACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAGGATAAGCTGGTTCTGTAC 198
              ||| |||||||||||||| |||| | |||||||||||||||||| |||||||| |||
Db        121 AACCTAAGCCTGGATGAGCTGGTCATATTTTGGCAGGACCAGGATAACCTGGTTCTCTAC 180

Qy        199 GAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGCAAGTATAAGGGCCGCACA 258
              ||||||||| ||||| ||||||| ||||| |||||| ||  |||||||| ||| ||||||
Db        181 GAGCTATACCGAGGCCAAGAGAAGCCTCATAATGTTAATTCCAAGTATATGGGTCGCACA 240

Qy        259 AGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATTCAGATCAAGGACAAGGGC 318
              ||||||||| | | ||  |||||||||||||||||| ||  |||| ||||||||||||||
Db        241 AGCTTTGACCAGGCCACCTGGACCCTGAGACTCCACAACGTTCAAATCAAGGACAAGGGC 300
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Qy        319 TTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTCGTTCCCATGCACCAGATG 378
Db        301 TCATATCAATGTTTCATCCATCATAAAGGGCCGCATGGACTTGTTCCTATCCACCAGATG 360

Qy        379 AATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAAATAATGGTAACTTCTAAT 438
Db        361 AGTTCTGACCTATCATTGCTTGCTAACTTCAGTCAACCTGAAATAAACCTACTTACTAAT 420

Qy        439 AGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCCATACAAGGTTACCCAGAA 498
Db        421 CACACAGAAAATTCTG---TCATAAATTTGACCTGCTCATCTACACAAGGCTACCCAGAA 477

Qy        499 CCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTAAGTATGATACTGTC 558
Db        478 CCCCAGAGGATGTATATGTTGCTAAATACGAAGAATTCAACCACTGAGCATGATGCTGAC 537

Qy        559 ATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTTTCTATCAGCTTGTCCTTC 618
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Qy        619 TCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGTCCTGCAACTTGAGTCAATGAA- 677
Db        598 CCCATCCCTCCCGAGACAAATGTGAGCATCGTCTGTGTCCTGCAACTTGAGCCAAGCAAG 657

Qy        678 -----GCTTCCCTCCCTACCTTATAATATAGATGCA---CATACGAAACCCACCCCTGAT 729
Db        658 ACACTGCTTTTCTCCCTACCTTGTAATATAGATGCAAAGCCACCTGTGCAACCCCCTGTC 717

Qy        730 GGAGACCACATCCTCTGGATTGCGGCTCTGCTTGTAATGTTGGTCATTTTGTGTGGGATG 789
Db        718 CCAGACCACATCCTCTGGATTGCAGCTCTACTTGTAACAGTGGTCGTTGTGTGTGGGATG 777

Qy        790 GTGTTCTTTCTAACACTAAGGAAAAGGAAGAAGAAGCAGCCTGGCCCCTCTCATGAAT-- 847
Db        778 GTGTCCTTTGTAACACTAAGGAAAAGGAAGAAGAAGCAGCCTGGCCCCTCTAATGAATGT 837

Qy        848 -GTGAAACCAACAAAGTGGAGAGAAAAGAAAGTGAGCAGACCAAGGAAAGAGTACGGTAC 906
Db        838 GGTGAAACCATCAAAATGAACAGGAAGGCGAGTGAACAAACTAAGAACAGAGCAGAAGTC 897

Qy        907 CATGAAACGGAAAGATCTGATGAAGCCCAGTG---TGTTAACATTTCGAAGACAGCTTCA 963
Db        898 CAT------GAACGATCTGATGATGCCCAGTGTGATGTTAATATTTTAAAGACAGCCTCA 951

Qy        964 GGCGACAACAGTACTACACAGTTT 987
Db        952 GATGACAACAGTACTACAGATTTT 975
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RESULT 9
BD237353

LOCUS	BD237353	994 bp DNA linear PAT 17-JUL-2003
DEFINITION	Improvement in tolerance to xenografts.	
ACCESSION	BD237353	
VERSION	BD237353.1 GI:33047123	
KEYWORDS	JP 2002532115-A/6.	
SOURCE	Sus sp.	
ORGANISM	Sus sp.	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
REFERENCE	1 (bases 1 to 994)	
AUTHORS	Lechler,R.I., Rogers,N.J. and Dorling,A.	
TITLE	Improvement in tolerance to xenografts	
JOURNAL	Patent: JP 2002532115-A 6 02-OCT-2002; ML LABORATORIES PLC	
COMMENT	OS Sus sp. (pig) PN JP 2002532115-A/6 PD 02-OCT-2002 PF 17-DEC-1999 JP 2000589212 PR 19-DEC-1998 GB 9827921.9,23-OCT-1999 GB 9925015.1 PI ROBERT IAN LECHLER,NICHOLA JANE ROGERS,ANTHONY DORLING PC C12N15/09,A61K39/00,A61P37/06,C07K16/28,C12P21/08,C12N15/00 CC Improvement in tolerance to xenografts	

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FH   Key             Location/Qualifiers
FT   source          1. .994
FT                   /organism='Sus sp. (pig)'.
FEATURES             Location/Qualifiers
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                     /organism="Sus sp."
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ORIGIN
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Query Match 62.8%; Score 620; DB 6; Length 994;
Best Local Similarity 81.3%; Pred. No. 8.7e-156;
Matches 800; Conservative 0; Mismatches 160; Indels 24; Gaps 6;

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Qy         19 ATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTCTATGGTGCTGCTTCCATG 78
Db          1 ATGGGACTGAGTAACATTCTCTTTGTGATGGTCCTCCTGCTCTCTGGTGCTGCCTCCTTG 60

Qy         79 AAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGCCATTTTACAAATTCTCAA 138
Db         61 AAAAGTCAGGCATATTTCAATGAGACTGGAGAACTGCCGTGCCATTTTACAAACTCGCAG 120

Qy        139 AACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAGGATAAGCTGGTTCTGTAC 198
Db        121 AACCTAAGCCTGGATGAGCTGGTCATATTTTGGCAGGACCAGGATAACCTGGTTCTCTAC 180

Qy        199 GAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGCAAGTATAAGGGCCGCACA 258
Db        181 GAGCTATACCGAGGCCAAGAGAAGCCTCATAATGTTAATTCCAAGTATATGGGTCGCACA 240

Qy        259 AGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATTCAGATCAAGGACAAGGGC 318
Db        241 AGCTTTGACCAGGCCACCTGGACCCTGAGACTCCACAACGTTCAAATCAAGGACAAGGGC 300

Qy        319 TTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTCGTTCCCATGCACCAGATG 378
Db        301 TCATATCAATGTTTCATCCATCATAAAGGGCCGCATGGACTTGTTCCTATCCACCAGATG 360

Qy        379 AATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAAATAATGGTAACTTCTAAT 438
Db        361 AGTTCTGACCTATCATTGCTTGCTAACTTCAGTCAACCTGAAATAAACCTACTTACTAAT 420

Qy        439 AGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCCATACAAGGTTACCCAGAA 498
Db        421 CACACAGAAAATTCTG---TCATAAATTTGACCTGCTCATCTACACAAGGCTACCCAGAA 477

Qy        499 CCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTAAGTATGATACTGTC 558
Db        478 CCCCAGAGGATGTATATGTTGCTAAATACGAAGAATTCAACCACTGAGCATGATGCTGAC 537

Qy        559 ATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTTTCTATCAGCTTGTCCTTC 618
Db        538 ATGAAGAAATCTCAAAATAACATCACGGAACTCTACAATGTATCAATCAGGGTGTCTCTT 597

Qy        619 TCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGTCCTGCAACTTGAGTCAATGAA- 677
Db        598 CCCATCCCTCCCGAGACAAATGTGAGCATCGTCTGTGTCCTGCAACTTGAGCCAAGCAAG 657

Qy        678 -----GCTTCCCTCCCTACCTTATAATATAGATGCA---CATACGAAACCCACCCCTGAT 729
Db        658 ACACTGCTTTTCTCCCTACCTTGTAATATAGATGCAAAGCCACCTGTGCAACCCCCTGTC 717

Qy        730 GGAGACCACATCCTCTGGATTGCGGCTCTGCTTGTAATGTTGGTCATTTTGTGTGGGATG 789
Db        718 CCAGACCACATCCTCTGGATTGCAGCTCTACTTGTAACAGTGGTCGTTGTGTGTGGGATG 777

Qy        790 GTGTTCTTTCTAACACTAAGGAAAAGGAAGAAGAAGCAGCCTGGCCCCTCTCATGAAT-- 847
Db        778 GTGTCCTTTGTAACACTAAGGAAAAGGAAGAAGAAGCAGCCTGGCCCCTCTAATGAATGT 837

Qy        848 -GTGAAACCAACAAAGTGGAGAGAAAAGAAAGTGAGCAGACCAAGGAAAGAGTACGGTAC 906
Db        838 GGTGAAACCATCAAAATGAACAGGAAGGCGAGTGAACAAACTAAGAACAGAGCAGAAGTC 897
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                     TQLLSSPFSIGTNTMEREESEQTKKREKINVPERSDEAQCVFKSLKTPSCDKSDTHF"
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     misc_feature    690
                     /note="144 nucleotide insertion in Homo sapiens CD86"
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  Query Match             62.0%;  Score 520.4;  DB 9;  Length 901;
  Best Local Similarity   79.0%;  Pred. No. 1.8e-127;
  Matches  659;  Conservative    0;  Mismatches  166;  Indels    9;  Gaps    3;

Qy         13 TGCACTATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTCTATGGTGCTGCT 72
              |||||||||| ||||| |||||||||||||||||| || |||||||| ||||||||||
Db          1 TGCACTATGGGACTGAGTAACATTCTCTTTGTGATGGCCTTCCTGCTCTCTGGTGCTGCT 60

Qy         73 TCCATGAAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGCCATTTTACAAAT 132
              || |||||| |||||| |||||||| |||||| ||| |||||||||| ||| ||||
Db         61 CCCCTGAAGATTCAAGCTTATTTCAATGAGACTGCAGACCTGCCATGCCAGTTTGCAAAC 120

Qy        133 TCTCAAAACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAGGATAAGCTGGTT 192
              |||||||| ||||||| |||| | ||||| |||||||| | ||||| || |||||
Db        121 TCTCAAAACCGAAGCCTGAGTGAGCTAGTAGTATTTTGGCAGAATCAGGAAAACTTGGTT 180

Qy        193 CTGTACGAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGCAAGTATAAGGGC 252
              ||| | ||| ||||| ||||| ||| ||   | | |  |||||| |||||||| ||||
Db        181 CTGAATGAGGTATACTTAGGCAGAGAAAAATTTGACAGCGTTCATTCCAAGTATATGGGC 240

Qy        253 CGCACAAGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATTCAGATCAAGGAC 312
              |||||||| |||||    || | |||||||||||| || || ||  ||||||||||||||
Db        241 CGCACAAGTTTTGATCCGGAGAGTTGGACCCTGAGGCTTCACAACCTTCAGATCAAGGAC 300

Qy        313 AAGGGCTTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTCGTTCCCATGCAC 372
              |||||||||||||||||| || | ||||| ||| |||||| |||| |  | | ||| |||
Db        301 AAGGGCTTGTATCAATGTATCATCCATCACAAAAGGCCCACAGGAATGATCCGCATCCAC 360

Qy        373 CAGATGAATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAAATAATGGTAACT 432
              |||||||||||||| || |||||||||||||| ||||||||||||||||||||    || |
Db        361 CAGATGAATTCTGAACTGTCAGTGCTTGCTAGCTTCAGTCAACCTGAAATAGTCCCAATT 420

Qy        433 TCTAATAGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCCATACAAGGTTAC 492
              ||||||| |||||||||   |      |||||||||||||||||||| ||||| ||||||
Db        421 TCTAATATAACAGAAAA---TATGTACATAAATTTGACCTGCTCATCTATACACGGTTAC 477

Qy        493 CCAGAACCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTAAGTATGAT 552
              |||||||  || |||||  | ||||| ||| |||| |||||||| ||   ||||||||
Db        478 CCAGAACCTGAGAAGATGAGTGTTTTGCTAAGAACCAAGAATTCAACTATCGAGTATGAT 537

Qy        553 ACTGTCATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTTTCTATCAGCTTG 612
              ||| ||| |||||||||| |||||||||||||||| ||| ||||||| |||||||||
Db        538 GGTGTTATGCAGAAATCTCAAGATAATGTCACAGAACTGTACGACGTTTCCATCAGCTTG 597

Qy        613 TCCTTCTCAGTCCCTGAAG---CAAGCAATGTGAGCATCTTCTGTGTCCTGCAACTTGAG 669
              ||  | ||| |||||||| |   | |||||  ||| |||||||||||| ||| ||  |||
Db        598 TCTGTTTCATTCCCTGATGTTACGAGCAACATGACCATCTTCTGTGTTCTGGAAACTGAC 657

Qy        670 TCAATGAAGCTTCCCTCCCTACCTTATAATATAGAAACCAACAAAGTGGAGAGAAAAGAA 729
                  |||||   |||  |||||     ||||| |||||||| | |||||||   ||||
Db        658 AAGACACAGCTTTTATCCTCACCTTTCTCTATAGGAACCAACACAATGGAGAGGGAAGAG 717

Qy        730 AGTGAGCAGACCAAGGAAAGAGTACGGTACCATGAAACGGAAAGATCTGATGAAGCCCAG 789
              ||||| ||||||||  ||||||  |      ||| | | ||||||||||||||||||||
Db        718 AGTGAACAGACCAAAAAAAGAGAAAAAATTAATGTACCTGAAAGATCTGATGAAGCCCAA 777

Qy        790 TGTG---TTAACATTTCGAAGACAGCTTCAGGCGACAACAGTACTACACAGTTT 840
              ||||   |||| | || ||||||| ||||| ||||||| |||  ||| || |||
Db        778 TGTGTTTTTAAAAGTTTGAAGACACCTTCATGCGACAAAAGTGATACGCATTTT 831


RESULT 9
PIGCD86G
LOCUS       PIGCD86G                  994 bp    mRNA    linear   MAM 17-JUN-1997
DEFINITION  Sus scrofa CD86 mRNA, complete cds.
ACCESSION   L76099
VERSION     L76099.1  GI:2198558
KEYWORDS    T cell costimulation.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 994)
  AUTHORS   Maher,S.E., Karmann,K., Min,W., Hughes,C.C., Pober,J.S. and
            Bothwell,A.L.
  TITLE     Porcine endothelial CD86 is a major costimulator of xenogeneic
            human T cells: cloning, sequencing, and functional expression in
            human endothelial cells
  JOURNAL   J. Immunol. 157 (9), 3838-3844 (1996)
  MEDLINE   97047772
   PUBMED   8892613
COMMENT     GSDB:S:74002
FEATURES             Location/Qualifiers
     source          1. .994
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /cell_line="PEC-A"
                     /cell_type="endothelial"
                     /clone_lib="3"
                     /dev_stage="adult"
     gene            1. .994
                     /gene="CD86"
     CDS             1. .978
                     /gene="CD86"
                     /standard_name="B7-2"
                     /note="putative"
                     /codon_start=1
                     /protein_id="AAB61307.1"
                     /db_xref="GI:2198559"
                     /translation="MGLSNILFVMVLLLSGAASLKSQAYFNETGELPCHFTNSQNLSL
                     DELVIFWQDQDNLVLYELYRGQEKPHNVNSKYMGRTSFDQATWTLRLHNVQIKDKGSY
                     QCFIHHKGPHGLVPIHQMSSDLSLLANFSQPEINLLTNHTENSVINLTCSSTQGYPEP
                     QRMYMLLNTKNSTTEHDADMKKSQNNITELYNVSIRVSLPIPPETNVSIVCVLQLEPS
                     KTLLFSLPCNIDAKPPVQPPVPDHILWIAALLVTVVVVCGMVSFVTLRKRKKKQPGPS
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     3'UTR           979. .994
                     /gene="CD86"
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                     /gene="CD86"
                     /evidence=experimental
ORIGIN

  Query Match             57.6%;  Score 484;  DB 4;  Length 994;
  Best Local Similarity   83.0%;  Pred. No. 8.5e-118;
  Matches  579;  Conservative    0;  Mismatches  110;  Indels    9;  Gaps    2;

Qy         19 ATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTCTATGGTGCTGCTTCCATG 78
              |||| ||||| |||||||||||||||||| |||||||||| |||||||| ||| ||
Db          1 ATGGGACTGAGTAACATTCTCTTTGTGATGGTCCTCCTGCTCTCTGGTGCTGCCTCCTTG 60

Qy         79 AAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGCCATTTTACAAATTCTCAA 138
              || ||||| |||||||||| |||||||||||||| |||||||||||||| || ||
Db         61 AAAAGTCAGGCATATTTCAATGAGACTGGAGAACTGCCGTGCCATTTTACAAACTCGCAG 120

Qy        139 AACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAGGATAAGCTGGTTCTGTAC 198
              ||| |||||||||||||| ||||  | |||||||||||||||||||| ||||||| |||
Db        121 AACCTAAGCCTGGATGAGCTGGTCATATTTTGGCAGGACCAGGATAACCTGGTTCTCTAC 180

Qy        199 GAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGCAAGTATAAGGGCCGCACA 258
              |||||||| ||||| ||||||| ||||| |||||| ||  |||||||| ||| ||||||
Db        181 GAGCTATACCGAGGCCAAGAGAAGCCTCATAATGTTAATTCCAAGTATATGGGTCGCACA 240

Qy        259 AGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATTCAGATCAAGGACAAGGGC 318
              |||||||| | | ||  |||||||||||||||||| ||  |||| ||||||||||||||
Db        241 AGCTTTGACCAGGCCACCTGGACCCTGAGACTCCACAACGTTCAAATCAAGGACAAGGGC 300

Qy        319 TTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTCGTTCCCATGCACCAGATG 378
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Db        301 TCATATCAATGTTTCATCCATCATAAAGGGCCGCATGGACTTGTTCCTATCCACCAGATG 360

Qy        379 AATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAAATAATGGTAACTTCTAAT 438

Db        361 AGTTCTGACCTATCATTGCTTGCTAACTTCAGTCAACCTGAAATAAACCTACTTACTAAT 420

Qy        439 AGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCCATACAAGGTTACCCAGAA 498

Db        421 CACACAGAAAATTCTG---TCATAAATTTGACCTGCTCATCTACACAAGGCTACCCAGAA 477

Qy        499 CCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTAAGTATGATACTGTC 558

Db        478 CCCCAGAGGATGTATATGTTGCTAAATACGAAGAATTCAACCACTGAGCATGATGCTGAC 537

Qy        559 ATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTTTCTATCAGCTTGTCCTTC 618

Db        538 ATGAAGAAATCTCAAAATAACATCACGGAACTCTACAATGTATCAATCAGGGTGTCTCTT 597

Qy        619 TCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGTCCTGCAACTTGAGTCAATGAA- 677

Db        598 CCCATCCCTCCCGAGACAAATGTGAGCATCGTCTGTGTCCTGCAACTTGAGCCAAGCAAG 657

Qy        678 -----GCTTCCCTCCCTACCTTATAATATAGAAACCAA 710

Db        658 ACACTGCTTTTCTCCCTACCTTGTAATATAGATGCAAA 695


RESULT 10
BD237353
LOCUS       BD237353                994 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Improvement in tolerance to xenografts.
ACCESSION   BD237353
VERSION     BD237353.1  GI:33047123
KEYWORDS    JP 2002532115-A/6.
SOURCE      Sus sp.
  ORGANISM  Sus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 994)
  AUTHORS   Lechler,R.I., Rogers,N.J. and Dorling,A.
  TITLE     Improvement in tolerance to xenografts
  JOURNAL   Patent: JP 2002532115-A 6 02-OCT-2002;
            ML LABORATORIES PLC
COMMENT     OS   Sus sp. (pig)
            PN   JP 2002532115-A/6
            PD   02-OCT-2002
            PF   17-DEC-1999 JP 2000589212
            PR   19-DEC-1998 GB    9827921.9,23-OCT-1999 GB    9925015.1 PI
            ROBERT IAN LECHLER,NICHOLA JANE ROGERS,ANTHONY DORLING PC
            C12N15/09,A61K39/00,A61P37/06,C07K16/28,C12P21/08,C12N15/00 CC
            Improvement in tolerance to xenografts
            FH   Key             Location/Qualifiers
            FT   source          1. .994
            FT                   /organism='Sus sp. (pig)'.
FEATURES              Location/Qualifiers
     source           1. .994
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  Query Match             57.6%;  Score 484;  DB 6;  Length 994;
  Best Local Similarity   83.0%;  Pred. No. 8.5e-118;
  Matches  579;  Conservative    0;  Mismatches  110;  Indels    9;  Gaps    2;

Qy         19 ATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTCTATGGTGCTGCTTCCATG 78

Db          1 ATGGGACTGAGTAACATTCTCTTTGTGATGGTCCTCCTGCTCTCTGGTGCTGCCTCCTTG 60

Qy         79 AAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGCCATTTTACAAATTCTCAA 138

Db         61 AAAAGTCAGGCATATTTCAATGAGACTGGAGAACTGCCGTGCCATTTTACAAACTCGCAG 120

Qy        139 AACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAGGATAAGCTGGTTCTGTAC 198

Db        121 AACCTAAGCCTGGATGAGCTGGTCATATTTTGGCAGGACCAGGATAACCTGGTTCTCTAC 180

Qy        199 GAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGCAAGTATAAGGGCCGCACA 258

Db        181 GAGCTATACCGAGGCCAAGAGAAGCCTCATAATGTTAATTCCAAGTATATGGGTCGCACA 240

Qy        259 AGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATTCAGATCAAGGACAAGGGC 318

Db        241 AGCTTTGACCAGGCCACCTGGACCCTGAGACTCCACAACGTTCAAATCAAGGACAAGGGC 300

Qy        319 TTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTCGTTCCCATGCACCAGATG 378

Db        301 TCATATCAATGTTTCATCCATCATAAAGGGCCGCATGGACTTGTTCCTATCCACCAGATG 360

Qy        379 AATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAAATAATGGTAACTTCTAAT 438

Db        361 AGTTCTGACCTATCATTGCTTGCTAACTTCAGTCAACCTGAAATAAACCTACTTACTAAT 420

Qy        439 AGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCCATACAAGGTTACCCAGAA 498

Db        421 CACACAGAAAATTCTG---TCATAAATTTGACCTGCTCATCTACACAAGGCTACCCAGAA 477

Qy        499 CCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTAAGTATGATACTGTC 558

Db        478 CCCCAGAGGATGTATATGTTGCTAAATACGAAGAATTCAACCACTGAGCATGATGCTGAC 537

Qy        559 ATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTTTCTATCAGCTTGTCCTTC 618

Db        538 ATGAAGAAATCTCAAAATAACATCACGGAACTCTACAATGTATCAATCAGGGTGTCTCTT 597

Qy        619 TCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGTCCTGCAACTTGAGTCAATGAA- 677

Db        598 CCCATCCCTCCCGAGACAAATGTGAGCATCGTCTGTGTCCTGCAACTTGAGCCAAGCAAG 657

Qy        678 -----GCTTCCCTCCCTACCTTATAATATAGAAACCAA 710

Db        658 ACACTGCTTTTCTCCCTACCTTGTAATATAGATGCAAA 695


RESULT 11
AX027016
LOCUS       AX027016                994 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 13 from Patent WO0037102.
ACCESSION   AX027016
VERSION     AX027016.1  GI:10188045
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1
  AUTHORS   Rogers,N.J., Dorling,A. and Lechler,R.I.
  TITLE     Immunosuppression
  JOURNAL   Patent: WO 0037102-A 13 29-JUN-2000;
            ROGERS NICHOLA JANE (GB) ; DORLING ANTHONY (GB) ; ML LAB PLC (GB) ;
            LECHLER ROBERT IAN (GB)
FEATURES              Location/Qualifiers
     source           1. .994
                      /organism="Sus scrofa"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9823"
ORIGIN

  Query Match             57.6%;  Score 484;  DB 6;  Length 994;
  Best Local Similarity   83.0%;  Pred. No. 8.5e-118;
  Matches  579;  Conservative    0;  Mismatches  110;  Indels    9;  Gaps    2;

Qy         19 ATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTCTATGGTGCTGCTTCCATG 78

Db          1 ATGGGACTGAGTAACATTCTCTTTGTGATGGTCCTCCTGCTCTCTGGTGCTGCCTCCTTG 60
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Qy        778 TTGTGTGGGATGGTGTTCTTTCTAACACTAAGGAAA---AGGAAGAAGAAGCAGCCTGGC 834
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Db        878 ATATGTGTGATGGTTTTCTGTCTAATTCTATGGAAATGGAAGAAGAAGAAGCGGCCTCGC 937

Qy        835 CCCTCTCATGAATGTGAAACCAACAAAGTGGAGAGAAAAGAAAGTGAGCAGACCAAGGAA 894
              |||| || |||||| |||||||| | |||||||  |||| |||||  ||||||||| ||
Db        938 AACTCTTATAAATGTGGAACCAACACAATGGAGAGGGAAGAGAGTGAACAGACCAAGAAA 997

Qy        895 AGAGTACGGTACCATGAAACGGAAAGATCTGATGAAGCCCAGTGTG---TTAACATTTCG 951
              |||| |     ||||  | | ||||||||||||||||||||| |||  |||| | ||||
Db        998 AGAGAAAAAATCCATATACCTGAAAGATCTGATGAAGCCCAGCGTGTTTTTAAAAGTTCG 1057

Qy        952 AAGACAGCTTCAGGCGACAACAGTACTACACAGTTT 987
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Db       1058 AAGACATCTTCATGCGACAAAAGTGATACATGTTTT 1093
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RESULT 9
US-08-479-744A-1
; Sequence 1, Application US/08479744A
; Patent No. 6084067
;  GENERAL INFORMATION:
;    APPLICANT:  Freeman, Gordon J.
;    APPLICANT:  Nadler, Lee M.
;    APPLICANT:  Gray, Gary S.
;    TITLE OF INVENTION:  No. 6084067el CTLA4/CD28 Ligands and
;    TITLE OF INVENTION:  Uses Therefor
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/479,744A
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/280,757
;      FILING DATE:  26-JUL-1994
;      APPLICATION NUMBER:  08/109,393
;      FILING DATE:  28-AUG-1993
;      APPLICATION NUMBER:  08/101,624
;      FILING DATE:  26-JULY-1993
;      APPLICATION NUMBER:  08/147,773
;      FILING DATE:  3-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  RPI-004CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1120 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  107..1093
US-08-479-744A-1
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  Query Match           58.3%;  Score 575.2;  DB 3;  Length 1120;
  Best Local Similarity  77.8%;  Pred. No. 6.3e-172;
  Matches  775;  Conservative    0;  Mismatches  203;  Indels   18;  Gaps    6;

Qy          1 ATGTATCTCAGATGCACTATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCTGCTC 60
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Db        107 ATGGATCCCCAGTGCACTATGGGACTGAGTAACATTCTCTTTGTGATGGCCTTCCTGCTC 166

Qy         61 TATGGTGCTGCTTCCATGAAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGC 120
              | |||||||||| |  |||||| |||||| ||||||||  |||||| ||| |||||||||
Db        167 TCTGGTGCTGCTCCTCTGAAGATTCAAGCTTATTTCAATGAGACTGCAGACCTGCCATGC 226

Qy        121 CATTTTACAAATTCTCAAAACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAG 180
              || ||| |||| |||||||||  |||||||  |||| | ||||| ||||||||||||||||
Db        227 CAATTTGCAAACTCTCAAAACCAAAGCCTGAGTGAGCTAGTAGTATTTTGGCAGGACCAG 286

Qy        181 GATAAGCTGGTTCTGTACGAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGC 240
              || ||  |||||||| | ||| |||||  ||||||||||||   | | | |||||||  |
Db        287 GAAAACTTGGTTCTGAATGAGGTATACTTAGGCAAAGAGAAATTTGACAGTGTTCATTCC 346

Qy        241 AAGTATAAGGGCCGCACAAGCTTTGACAAAGACAATTGGACCCTGAGACTCCATAATATT 300
              ||||||| |||||||||||| |||||   |||| |||||||||||||||| || ||| ||
Db        347 AAGTATATGGGCCGCACAAGTTTTGATTCGGACAGTTGGACCCTGAGACTTCACAATCTT 406

Qy        301 CAGATCAAGGACAAGGGCTTGTATCAATGTTTCGTTCATCATAAAGGGCCCAAAGGACTC 360
              |||||||||||||||||||||||||||| || | ||||| |||  ||||| |||| | |
Db        407 CAGATCAAGGACAAGGGCTTGTATCAATGTATCATCCATCACAAAAAGCCCACAGGAATG 466

Qy        361 GTTCCCATGCACCAGATGAATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAA 420
              ||| |||| |||||||||||||||| || |||||||||||||||||||||||||||||||
Db        467 ATTCGCATCCACCAGATGAATTCTGAACTGTCAGTGCTTGCTAACTTCAGTCAACCTGAA 526

Qy        421 ATAATGGTAACTTCTAATAGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCC 480
              |||  |   || |||||||| |||||||||   ||    |||||||||||||||||||
Db        527 ATAGTACCAATTTCTAATATAACAGAAAA---TGTGTACATAAATTTGACCTGCTCATCT 583

Qy        481 ATACAAGGTTACCCAGAACCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGT 540
              ||||| |||||||||||||| ||| |||||  | ||||| ||| |||| |||||||||| |
Db        584 ATACACGGTTACCCAGAACCTAAGAAGATGAGTGTTTTGCTAAGAACCAAGAATTCAACT 643

Qy        541 ACTAAGTATGATACTGTCATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTT 600
              |   |||||||| | | ||| |||||||||| |||||||||||||||| ||| |||||
Db        644 ATCGAGTATGATGGTATTATGCAGAAATCTCAAGATAATGTCACAGAACTGTACGACGTT 703

Qy        601 TCTATCAGCTTGTCCTTCTCAGTCCCTGAAG---CAAGCAATGTGAGCATCTTCTGTGTC 657
              || |||||||||||  | ||| |||||| |   | |||||| ||| |||||||||| |
Db        704 TCCATCAGCTTGTCTGTTTCATTCCCTGATGTTACGAGCAATATGACCATCTTCTGTATT 763

Qy        658 CTGCAACTTGAGTCAATGAAGCTTCCCTCCCTACCTTATAATATAGATGCACATACGAAA 717
              ||| ||  |||  | |  |||| ||  |||||    ||||||    | |  | |
Db        764 CTGGAAACTGACAAGACGCGGCTTTTATCTTCACCTTTCTCTATAGA---GCTTGAGGAC 820

Qy        718 CCCACCCCTGATGGAGACCACATCCTCTGGATTGCGGCTCTGCTTGTAATGTTGGTCATT 777
              ||     |||       |||||||||  |  |||||  | |||  | |||   ||     || |||
Db        821 CCTCAGCCTCCCCCAGACCACATTCCTTGGATTACAGCTGTACTTCCAA---CAGTTATT 877

Qy        778 TTGTGTGGGATGGTGTTCTTTCTAACACTAAGGAAA---AGGAAGAAGAAGCAGCCTGGC 834
              | |||| |||||| |||| |||||  ||| |||||   | ||||||||||| |||| ||
Db        878 ATATGTGTGATGGTTTTCTGTCTAATTCTATGGAAATGGAAGAAGAAGAAGCGGCCTCGC 937

Qy        835 CCCTCTCATGAATGTGAAACCAACAAAGTGGAGAGAAAAGAAAGTGAGCAGACCAAGGAA 894
              |||| || |||||| |||||||| | |||||||  |||| |||||  ||||||||| ||
Db        938 AACTCTTATAAATGTGGAACCAACACAATGGAGAGGGAAGAGAGTGAACAGACCAAGAAA 997

Qy        895 AGAGTACGGTACCATGAAACGGAAAGATCTGATGAAGCCCAGTGTG---TTAACATTTCG 951
              |||| |     ||||  | | ||||||||||||||||||||| |||  |||| | ||||
Db        998 AGAGAAAAAATCCATATACCTGAAAGATCTGATGAAGCCCAGCGTGTTTTTAAAAGTTCG 1057

Qy        952 AAGACAGCTTCAGGCGACAACAGTACTACACAGTTT 987
              |||||| ||||| ||||||| |||  ||||   |||
Db       1058 AAGACATCTTCATGCGACAAAAGTGATACATGTTTT 1093
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                :||| |:|||||| || ||| :| |||||:| :||| | |||| || |||||||||: |
Db          4 QCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNQSLSELVVFWQDQENL 63

Qy         64 VLYELYRGKENPQNVHRKYKGRTSFDKDNWTLRLHNIQIKDKGLYQCFVHHKGPKGLVPM 123
               || |:| |||   :|| || |||||| |:||||||:|||||||||| :||| | |:: :
Db         64 VLNEVYLGKEKFDSVHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRI 123

Qy        124 HQMNSDLSVLANFSQPEIMVTSNRTENSGIINLTCSSIQGYPEPKEMYFLVKTENSSTKY 183
               |||||:|||||||||||:  || |||   |||||||| |||||||:|  |::|:||: :|
Db        124 HQMNSELSVLANFSQPEIVPISNITENV-YINLTCSSIHGYPEPKKMSVLLRTKNSTIEY 182

Qy        184 DTVMKKSQNNVTELYNVSISLSFSVPE-ASNVSIFCVLQLESMKLPSLPYNIDAHTKPTP 242
               | :|:|||:||||||:|||||| | |:  ||::|||:|: :  :| | |::|:     | |
Db        183 DGIMQKSQDNVTELYDVSISLSVSFPDVTSNMTIFCILETDKTRLLSSPFSIELE-DPQP 241

Qy        243 DGDHILWIAALLVMLVILCGMVFFLTLRK-RKKKQPGPSHECETNKVERKESEQTKERVR 301
                 ||| || |:|   ||:| ||| | | | :|||:|  |::| || :||:||||||:| :
Db        242 PPDHIPWITAVL-PTVIICVMVFCLILWKWKKKKRPRNSYKCGTNTMEREESEQTKKREK 300

Qy        302 YHETERSDEAQCV-NISKTASGDNSTTQF 329
                |  ||||||| |   |||:| | | | |
Db        301 IHIPERSDEAQRVFKSSKTSSCDKSDTCF 329
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RESULT 7
US-08-479-744A-2
; Sequence 2, Application US/08479744A
; Patent No. 6084067
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-479-744A-2

Query Match 57.9%; Score 1003; DB 3; Length 329;
Best Local Similarity 62.3%; Pred. No. 1e-93;
Matches 205; Conservative 47; Mismatches 71; Indels 6; Gaps 6;

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Qy          4 RCTMELNNILFVMTLLLYGAASMKSQAYFNKTGELPCHFTNSQNISLDELVVFWQDQDKL 63
               :||| |:|||||  || ||| :| |||||:| :||| | |||| || |||||||||: |
Db          4 QCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNQSLSELVVFWQDQENL 63

Qy         64 VLYELYRGKENPQNVHRKYKGRTSFDKDNWTLRLHNIQIKDKGLYQCFVHHKGPKGLVPM 123
               || |:| |||   :|| || |||||| |:||||||:|||||||||| :||| | |:: :
Db         64 VLNEVYLGKEKFDSVHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRI 123

Qy        124 HQMNSDLSVLANFSQPEIMVTSNRTENSGIINLTCSSIQGYPEPKEMYFLVKTENSSTKY 183
               |||||:|||||||||||:  || |||   |||||||| |||||||:|  |::|:||: :|
Db        124 HQMNSELSVLANFSQPEIVPISNITENV-YINLTCSSIHGYPEPKKMSVLLRTKNSTIEY 182

Qy        184 DTVMKKSQNNVTELYNVSISLSFSVPE-ASNVSIFCVLQLESMKLPSLPYNIDAHTKPTP 242
               | :|:|||:||||||:|||||| | |:  ||::|||:|: :  :| | |::|:     | |
Db        183 DGIMQKSQDNVTELYDVSISLSVSFPDVTSNMTIFCILETDKTRLLSSPFSIELE-DPQP 241

Qy        243 DGDHILWIAALLVMLVILCGMVFFLTLRK-RKKKQPGPSHECETNKVERKESEQTKERVR 301
                 ||| || |:|   ||:| ||| | | | :|||:|  |::| || :||:||||||:| :
Db        242 PPDHIPWITAVL-PTVIICVMVFCLILWKWKKKKRPRNSYKCGTNTMEREESEQTKKREK 300

Qy        302 YHETERSDEAQCV-NISKTASGDNSTTQF 329
                |  ||||||| |   |||:| | | | |
Db        301 IHIPERSDEAQRVFKSSKTSSCDKSDTCF 329
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RESULT 8
US-08-280-757B-2
; Sequence 2, Application US/08280757B
; Patent No. 6130316
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; APPLICANT: Greenfield, Edward
; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/280,757B
; FILING DATE: 26-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941